



SEQUENCE LISTING

<110> KIM, DO-MAN
KANG, HEE-KYOUNG
LEE, JIN-HA

<120> PROTEIN WITH ACTIVITY OF HYDROLYZING DEXTRAN, STARCH,
MUTAN, INULIN, AND LEVAN, GENE ENCODING THE SAME, CELL
EXPRESSING THE SAME, AND PRODUCTION METHOD THEREOF

<130> 44352-0010-00-US

<140> 10/588,140

<141> 2006-07-31

<150> PCT/KR05/00234

<151> 2005-01-27

<150> KR 10-2004-0006185

<151> 2004-01-30

<160> 9

<170> PatentIn Ver. 3.3

<210> 1

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
construct

<400> 1

Met Thr Leu Ile Tyr Val Pro Ser Ile Phe Thr Met Val Pro Ser Ile
1 5 10 15

Thr Arg Ile Val Leu Val Asn Ile Leu Leu Ala Thr Leu Val Leu Gly
20 25 30

Ala Ala Val Leu Pro Arg Asp Asn Arg Thr Val Cys Gly Ser Gln Leu
35 40 45

Cys Thr Trp Trp His Asp Ser Gly Glu Ile Asn Thr Gly Thr Pro Val
50 55 60

Gln Ala Gly Asn Val Arg Gln Ser Arg Lys Tyr Ser Val His Val Ser
65 70 75 80

Leu Ala Asp Arg Asn Gln Phe Tyr Asp Ser Phe Val Tyr Glu Ser Ile
85 90 95

Pro Arg Asn Gly Asn Gly Arg Ile Tyr Ser Pro Thr Asp Pro Pro Asn
100 105 110

Ser Asn Thr Leu Asn Ser Ser Ile Asp Asp Gly Ile Ser Ile Glu Pro
115 120 125

Ser Leu Gly Ile Asn Met Ala Trp Ser Gln Phe Glu Tyr Arg Arg Asp
 130 135 140
 Val Asp Ile Lys Ile Thr Thr Ile Asp Gly Ser Ile Leu Asp Gly Pro
 145 150 155 160
 Leu Asp Ile Val Ile Arg Pro Thr Ser Val Lys Tyr Ser Val Lys Arg
 165 170 175
 Cys Val Gly Gly Ile Ile Ile Arg Val Pro Tyr Asp Pro Asn Gly Arg
 180 185 190
 Lys Phe Ser Val Glu Leu Lys Ser Asp Leu Tyr Ser Tyr Leu Ser Asp
 195 200 205
 Gly Ser Gln Tyr Val Thr Ser Gly Gly Ser Val Val Gly Val Glu Pro
 210 215 220
 Lys Asn Ala Leu Val Ile Phe Ala Ser Pro Phe Leu Pro Arg Asp Met
 225 230 235 240
 Val Pro His Met Thr Pro His Asp Thr Gln Thr Met Lys Pro Gly Pro
 245 250 255
 Ile Asn Asn Gly Asp Trp Gly Ser Lys Pro Ile Leu Tyr Phe Pro Pro
 260 265 270
 Gly Val Tyr Trp Met Asn Glu Asp Thr Ser Gly Asn Pro Gly Lys Leu
 275 280 285
 Gly Ser Asn His Met Arg Leu Asp Pro Asn Thr Tyr Trp Val His Leu
 290 295 300
 Ala Pro Gly Ala Tyr Val Lys Gly Ala Ile Glu Tyr Phe Thr Lys Gln
 305 310 315 320
 Asn Phe Tyr Ala Thr Gly His Gly Val Leu Ser Gly Glu Asn Tyr Val
 325 330 335
 Tyr Gln Ala Asn Ala Ala Asp Asn Tyr Tyr Ala Val Lys Ser Asp Gly
 340 345 350
 Thr Ser Leu Arg Met Trp Trp His Asn Asn Leu Gly Gly Gly Gln Thr
 355 360 365
 Trp Phe Cys Met Gly Pro Thr Ile Asn Ala Pro Pro Phe Asn Thr Met
 370 375 380
 Asp Phe Asn Gly Asn Ser Asn Ile Ser Ser Arg Ile Ser Asp Tyr Lys
 385 390 395 400
 Gln Val Gly Ala Tyr Phe Phe Gln Thr Asp Gly Pro Glu Ile Tyr Glu
 405 410 415
 Asp Ser Val Val His Asp Val Phe Trp His Val Asn Asp Asp Ala Ile
 420 425 430

Lys Thr Tyr Tyr Ser Gly Ala Ser Ile Ser Arg Ala Thr Ile Trp Lys
 435 440 445

Cys His Asn Asp Pro Ile Ile Gln Met Gly Trp Thr Ser Arg Asn Leu
 450 455 460

Thr Gly Ile Ser Ile Asp Asn Leu His Val Ile His Thr Arg Tyr Phe
 465 470 475 480

Lys Ser Glu Thr Val Val Pro Ser Ala Ile Ile Gly Ala Ser Pro Phe
 485 490 495

Tyr Ala Ser Gly Met Thr Val Asp Pro Ser Glu Ser Ile Ser Met Thr
 500 505 510

Ile Ser Asn Val Val Cys Glu Gly Leu Cys Pro Ser Leu Phe Arg Ile
 515 520 525

Thr Pro Leu Gln Ser Tyr Asn Asn Leu Val Val Lys Asn Val Ala Phe
 530 535 540

Pro Asp Gly Leu Gln Thr Asn Pro Ile Gly Ile Gly Glu Ser Ile Ile
 545 550 555 560

Pro Ala Ala Ser Gly Cys Thr Met Asp Leu Glu Ile Thr Asn Trp Thr
 565 570 575

Val Lys Gly Gln Lys Val Thr Met Gln Asn Phe Gln Ser Gly Ser Leu
 580 585 590

Gly Gln Phe Asp Ile Asp Gly Ser Tyr Trp Gly Gln Trp Ser Ile Asn
 595 600 605

<210> 2

<211> 2052

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 construct

<220>

<221> CDS

<222> (42)..(1865)

<400> 2

tggtgtgtgc ccttgctctg ccaacgttgt tgattgtttt c atg aca tta atc tac 56
 Met Thr Leu Ile Tyr
 1 5

gtg cct tca ata ttt aca atg gtc ccc tca atc aca cgg att gta ctg 104
 Val Pro Ser Ile Phe Thr Met Val Pro Ser Ile Thr Arg Ile Val Leu
 10 15 20

gtt aac att ctg ttg gcg acg ttg gtt ttg gga gct gca gtc ctt cca	152
Val Asn Ile Leu Leu Ala Thr Leu Val Leu Gly Ala Ala Val Leu Pro	
25 30 35	
cga gac aac aga act gtt tgc ggg agt caa ctc tgc aca tgg tgg cac	200
Arg Asp Asn Arg Thr Val Cys Gly Ser Gln Leu Cys Thr Trp Trp His	
40 45 50	
gac tcc ggc gag ata aac acc ggt act cct gta cag gca gga aac gtt	248
Asp Ser Gly Glu Ile Asn Thr Gly Thr Pro Val Gln Ala Gly Asn Val	
55 60 65	
cga caa tcc cga aag tac tct gtc cat gtg agc ctg gca gac cgt aac	296
Arg Gln Ser Arg Lys Tyr Ser Val His Val Ser Leu Ala Asp Arg Asn	
70 75 80 85	
caa ttc tac gac tct ttc gta tat gaa tgc ata cct agg aac ggc aat	344
Gln Phe Tyr Asp Ser Phe Val Tyr Glu Ser Ile Pro Arg Asn Gly Asn	
90 95 100	
ggc aga att tat tct ccc acc gac cca cct aac agc aat aca ttg aat	392
Gly Arg Ile Tyr Ser Pro Thr Asp Pro Pro Asn Ser Asn Thr Leu Asn	
105 110 115	
agt agc att gac gac ggt ata tca atc gaa cca tct ctc ggc atc aac	440
Ser Ser Ile Asp Asp Gly Ile Ser Ile Glu Pro Ser Leu Gly Ile Asn	
120 125 130	
atg gct tgg tcc cag ttc gaa tat aga cga gat gtc gac att aag att	488
Met Ala Trp Ser Gln Phe Glu Tyr Arg Arg Asp Val Asp Ile Lys Ile	
135 140 145	
act aca atc gat ggc tca ata ttg gat ggc cct ttg gac att gtt att	536
Thr Thr Ile Asp Gly Ser Ile Leu Asp Gly Pro Leu Asp Ile Val Ile	
150 155 160 165	
cgg ccg act tct gtt aag tac tca gtc aaa aga tgt gtg ggt ggt atc	584
Arg Pro Thr Ser Val Lys Tyr Ser Val Lys Arg Cys Val Gly Gly Ile	
170 175 180	
att att aga gtc cct tat gat ccc aat ggt cga aaa ttc tct gtt gag	632
Ile Ile Arg Val Pro Tyr Asp Pro Asn Gly Arg Lys Phe Ser Val Glu	
185 190 195	
tta aag agt gac ctt tac agt tac ctc tcc gac ggt tgc caa tat gtg	680
Leu Lys Ser Asp Leu Tyr Ser Tyr Leu Ser Asp Gly Ser Gln Tyr Val	
200 205 210	
acc tct gga ggg agc gtg gtt ggt gtg gag cca aaa aat gcc ctg gtg	728
Thr Ser Gly Gly Ser Val Val Gly Val Glu Pro Lys Asn Ala Leu Val	
215 220 225	
atc ttt gcc agc cct ttc ttg cca cgg gat atg gtt cct cat atg aca	776
Ile Phe Ala Ser Pro Phe Leu Pro Arg Asp Met Val Pro His Met Thr	
230 235 240 245	

cca cac gac acc cag aca atg aag ccg ggc cca atc aat aat ggg gac	824
Pro His Asp Thr Gln Thr Met Lys Pro Gly Pro Ile Asn Asn Gly Asp	
250 255 260	
tggtgggt tca aag cct ata ctc tac ttc ccg cct ggc gta tac tgg atg	872
Trp Gly Ser Lys Pro Ile Leu Tyr Phe Pro Pro Gly Val Tyr Trp Met	
265 270 275	
aac gag gat acc tct ggt aac ccc ggg aag ctc ggc tca aat cat atg	920
Asn Glu Asp Thr Ser Gly Asn Pro Gly Lys Leu Gly Ser Asn His Met	
280 285 290	
cggtctg gat ccc aat acc tac tgg gtc cat cta gcc cca gga gcc tat	968
Arg Leu Asp Pro Asn Thr Tyr Trp Val His Leu Ala Pro Gly Ala Tyr	
295 300 305	
gtgaaa gga gcc att gag tat ttc acg aag caa aat ttc tat gca acg	1016
Val Lys Gly Ala Ile Glu Tyr Phe Thr Lys Gln Asn Phe Tyr Ala Thr	
310 315 320 325	
gggtcat ggc gtt ctc tca ggt gag aac tat gtt tat cag gcc aat gca	1064
Gly His Gly Val Leu Ser Gly Glu Asn Tyr Val Tyr Gln Ala Asn Ala	
330 335 340	
gctgat aac tac tat gcc gtc aag agt gat ggc aca agc ttg aga atg	1112
Ala Asp Asn Tyr Tyr Ala Val Lys Ser Asp Gly Thr Ser Leu Arg Met	
345 350 355	
tggtgg cac aac aac ctt gga ggc ggt caa aca tgg ttt tgc atg ggg	1160
Trp Trp His Asn Asn Leu Gly Gly Gly Gln Thr Trp Phe Cys Met Gly	
360 365 370	
cccacc att aat gca ccg ccg ttt aat acg atg gac ttc aac gga aac	1208
Pro Thr Ile Asn Ala Pro Pro Phe Asn Thr Met Asp Phe Asn Gly Asn	
375 380 385	
tctaat att tcc agc cgg att agt gac tat aag cag gtt ggc gct tat	1256
Ser Asn Ile Ser Ser Arg Ile Ser Asp Tyr Lys Gln Val Gly Ala Tyr	
390 395 400 405	
tttttc caa aca gac gga ccg gag atc tac gag gac agt gtt gtc cat	1304
Phe Phe Gln Thr Asp Gly Pro Glu Ile Tyr Glu Asp Ser Val Val His	
410 415 420	
gacgtc ttc tgg cat gtt aat gat gat gcc atc aag aca tat tat tcc	1352
Asp Val Phe Trp His Val Asn Asp Asp Ala Ile Lys Thr Tyr Tyr Ser	
425 430 435	
ggagct tca att tca cga gca acc atc tgg aag tgt cac aat gac ccg	1400
Gly Ala Ser Ile Ser Arg Ala Thr Ile Trp Lys Cys His Asn Asp Pro	
440 445 450	
atcata cag atg ggc tgg acg tca cga aat ctc acc gga atc agc att	1448
Ile Ile Gln Met Gly Trp Thr Ser Arg Asn Leu Thr Gly Ile Ser Ile	
455 460 465	

gat aac ctg cac gtc atc cac acg aga tat ttc aaa tct gaa aca gtg 1496
 Asp Asn Leu His Val Ile His Thr Arg Tyr Phe Lys Ser Glu Thr Val
 470 475 480 485

gtt cct tca gca atc att gga gcg tct cca ttc tac gca agt gga atg 1544
 Val Pro Ser Ala Ile Ile Gly Ala Ser Pro Phe Tyr Ala Ser Gly Met
 490 495 500

act gtt gat ccc agc gag tcc atc agc atg acc atc tct aac gtg gtg 1592
 Thr Val Asp Pro Ser Glu Ser Ile Ser Met Thr Ile Ser Asn Val Val
 505 510 515

tgt gag ggt cta tgc ccc tca ctg ttc cgt atc act ccg ctt cag agc 1640
 Cys Glu Gly Leu Cys Pro Ser Leu Phe Arg Ile Thr Pro Leu Gln Ser
 520 525 530

tac aac aac ctt gtt gtc aag aac gtg gcc ttt ccc gat gga ctg cag 1688
 Tyr Asn Asn Leu Val Val Lys Asn Val Ala Phe Pro Asp Gly Leu Gln
 535 540 545

aca aat cca atc gga ata gga gag agc att ata cca gca gct tcc ggc 1736
 Thr Asn Pro Ile Gly Ile Gly Glu Ser Ile Ile Pro Ala Ala Ser Gly
 550 555 560 565

tgt aca atg gac ttg gaa atc aca aac tgg acc gtc aaa gga caa aaa 1784
 Cys Thr Met Asp Leu Glu Ile Thr Asn Trp Thr Val Lys Gly Gln Lys
 570 575 580

gtc acc atg caa aac ttt cag tcc ggg tca ctt ggc cag ttc gat atc 1832
 Val Thr Met Gln Asn Phe Gln Ser Gly Ser Leu Gly Gln Phe Asp Ile
 585 590 595

gat ggt tca tac tgg ggt caa tgg tcc ata aac taaagctatt cccattcacc 1885
 Asp Gly Ser Tyr Trp Gly Gln Trp Ser Ile Asn
 600 605

tgagtatttt cgtgggttca atgagttctt gttactgatg gggcccttgc tagtggtaaa 1945

agtagaggga cttgtcctcg ccgggcgcca aggaagttca tgtcttctag ttgaatagta 2005

tttgtttctt ctctctcgtt aaaaaaaaaa aaaaaaaaaa aaaaaaa 2052

<210> 3

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 3

gtcccttgag ctcccaac

<210> 4
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 4
 tcaactagaa ttcatgaact tcc

23

<210> 5
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 5
 gagagagaga gagagagaga actagtctcg agtttttttt tttttttttt

50

<210> 6
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 6
 acctggcaya grdmm

15

<210> 7
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 7
 gsykccsacc tgcttrta

18

<210> 8
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (5)
<223> Asp or Asn

<220>
<221> MOD_RES
<222> (6)
<223> Asn, Ser or Thr

<400> 8
Thr Trp Trp His Xaa Xaa
1 5

<210> 9
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (6)
<223> Ser or Ala

<400> 9
Tyr Lys Gln Val Gly Xaa
1 5